

Towards understanding RAV1 transcriptional network during the growth-dormancy cycle in poplar

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As plants are sessile organisms, the decision to grow or to stop growing is fundamental for their survival. To survive to the harsh condition of the winter, temperate and boreal trees undergo a self-protective developmental reprogramming known as winter dormancy. Its mechanism involves an intricate interplay between endogenous growth regulators and the winter external signal, such as shortening of photoperiod and cold temperatures. Currently, only few factors including circadian and developmental transcription factors and hormonal signaling molecules have been shown to modulate the extension of the dormancy period in woody plants. In our laboratory, the circadian controlled transcription factor RAV promotes sylleptic branching and reduces dormancy length when RAV is ectopic overexpressed in poplar (1). Comparative mRNA profiling of RAV overexpressing versus wild type revealed a transcriptional rearrangement happens as effect of constitutive high level of RAV, giving rise to phenology. However, to define RAV mode of action as a transcriptional regulator and how RAV activity trigger a modification of dormancy-growth cycle, its primary targets genes should be investigated. At this particular, the translational fusion of a given transcription factor to the rat glucocorticoid receptor domain (GR) have been widely used in Arabidopsis and recently in poplar (2). In this work we show the standardization of a methodology required to identify primary target genes for a transcription factor in poplar. This will be useful to future exploration of RAV1 gene network and its mode of action in spatio-temporal studies at tissue level during growth-dormancy cycle in poplar.

References

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Funding

This work is funded by the Spanish Ministerio de Ciencia e Innovación AGL2011-22625/FOR for I.A. Marie Curie Actions - Support for training and career development of researcher (CIG) (PCIG13-GA-2013-631630) and Ramon y Cajal fellowship from the Spanish Ministerio de Economía y Competitividad (RYC-2012-10194) for M.P.